

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Loeb, Lawrence A.
Hood, Leroy
Suzuki, Motoshi
- (ii) TITLE OF INVENTION: Thermostable Polymerases Having Altered Fidelity and Methods of Identifying and Using Same
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: CAMPBELL & FLORES LLP
 - (B) STREET: 4370 La Jolla Village Drive, Suite 700
 - (C) CITY: San Diego
 - (D) STATE: California
 - (E) COUNTRY: United States
 - (F) ZIP: 92121
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/978,806
 - (B) FILING DATE: 26-NOV-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/031,496
 - (B) FILING DATE: 27-NOV-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Campbell, Cathryn A.
 - (B) REGISTRATION NUMBER: 31,815
 - (C) REFERENCE/DOCKET NUMBER: P-UW 2873
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2626 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 121..2616

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTCAGAT CTACCTGCCT GAGGGCGTCC GGTTCCAGCT GGCCCTTCCC GAGGGGGAGA	60
GGGAGGCGTT TCTAAAAGCC CTTCAGGACG CTACCCGGGG GCGGGTGGTG GAAGGGTAAC	120

ATG AGG GGG ATG CTG CCC CTC TTT GAG CCC AAG GGC CGG GTC CTC CTG	168
Met Arg Gly Met Leu Pro Leu Phe Glu Pro Lys Gly Arg Val Leu Leu	
1 5 10 15	
GTG GAC GGC CAC CAC CTG GCC TAC CGC ACC TTC CAC GCC CTG AAG GGC	216
Val Asp Gly His His Leu Ala Tyr Arg Thr Phe His Ala Leu Lys Gly	
20 25 30	
CTC ACC ACC AGC CGG GGG GAG CCG GTG CAG GCG GTC TAC GGC TTC GCC	264
Leu Thr Thr Ser Arg Gly Glu Pro Val Gln Ala Val Tyr Gly Phe Ala	
35 40 45	
AAG AGC CTC CTC AAG GCC CTC AAG GAG GAC GGG GAC GCG GTG ATC GTG	312
Lys Ser Leu Leu Lys Ala Leu Lys Glu Asp Gly Asp Ala Val Ile Val	
50 55 60	
GTC TTT GAC GCC AAG GCC CCC TCC TTC CGC CAC GAG GCC TAC GGG GGG	360
Val Phe Asp Ala Lys Ala Pro Ser Phe Arg His Glu Ala Tyr Gly Gly	
65 70 75 80	
TAC AAG GCG GGC CGG GCC CCC ACG CCG GAG GAC TTT CCC CGG CAA CTC	408
Tyr Lys Ala Gly Arg Ala Pro Thr Pro Glu Asp Phe Pro Arg Gln Leu	
85 90 95	
GCC CTC ATC AAG GAG CTG GTG GAC CTC CTG GGG CTG GCG CGC CTC GAG	456
Ala Leu Ile Lys Glu Leu Val Asp Leu Leu Gly Leu Ala Arg Leu Glu	
100 105 110	
GTC CCG GGC TAC GAG GCG GAC GAC GTC CTG GCC AGC CTG GCC AAG AAG	504
Val Pro Gly Tyr Glu Ala Asp Asp Val Leu Ala Ser Leu Ala Lys Lys	
115 120 125	
GCG GAA AAG GAG GGC TAC GAG GTC CGC ATC CTC ACC GCC GAC AAA GAC	552
Ala Glu Lys Glu Gly Tyr Glu Val Arg Ile Leu Thr Ala Asp Lys Asp	
130 135 140	
CTT TAC CAG CTC CTT TCC GAC CGC ATC CAC GTC CTC CAC CCC GAG GGG	600
Leu Tyr Gln Leu Leu Ser Asp Arg Ile His Val Leu His Pro Glu Gly	
145 150 155 160	
TAC CTC ATC ACC CCG GCC TGG CTT TGG GAA AAG TAC GGC CTG AGG CCC	648
Tyr Leu Ile Thr Pro Ala Trp Leu Trp Glu Lys Tyr Gly Leu Arg Pro	
165 170 175	
GAC CAG TGG GCC GAC TAC CGG GCC CTG ACC GGG GAC GAG TCC GAC AAC	696
Asp Gln Trp Ala Asp Tyr Arg Ala Leu Thr Gly Asp Glu Ser Asp Asn	
180 185 190	
CTT CCC GGG GTC AAG GGC ATC GGG GAG AAG ACG GCG AGG AAG CTT CTG	744
Leu Pro Gly Val Lys Gly Ile Gly Glu Lys Thr Ala Arg Lys Leu Leu	
195 200 205	
GAG GAG TGG GGG AGC CTG GAA GCC CTC CTC AAG AAC CTG GAC CGG CTG	792
Glu Glu Trp Gly Ser Leu Glu Ala Leu Leu Lys Asn Leu Asp Arg Leu	
210 215 220	
AAG CCC GCC ATC CGG GAG AAG ATC CTG GCC CAC ATG GAC GAT CTG AAG	840
Lys Pro Ala Ile Arg Glu Lys Ile Leu Ala His Met Asp Asp Leu Lys	
225 230 235 240	
CTC TCC TGG GAC CTG GCC AAG GTG CGC ACC GAC CTG CCC CTG GAG GTG	888
Leu Ser Trp Asp Leu Ala Lys Val Arg Thr Asp Leu Pro Leu Glu Val	
245 250 255	
GAC TTC GCC AAA AGG CGG GAG CCC GAC CGG GAG AGG CTT AGG GCC TTT	936
Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe	
260 265 270	

CTG	GAG	AGG	CTT	GAG	TTT	GGC	AGC	CTC	CTC	CAC	GAG	TTC	GGC	CTT	CTG	984
Leu	Glu	Arg	Leu	Glu	Phe	Gly	Ser	Leu	Leu	His	Glu	Phe	Gly	Leu	Leu	
		275					280					285				
GAA	AGC	CCC	AAG	GCC	CTG	GAG	GAG	GCC	CCC	TGG	CCC	CCG	CCG	GAA	GGG	1032
Glu	Ser	Pro	Lys	Ala	Leu	Glu	Glu	Ala	Pro	Trp	Pro	Pro	Pro	Glu	Gly	
		290				295					300					
GCC	TTC	GTG	GGC	TTT	GTG	CTT	TCC	CGC	AAG	GAG	CCC	ATG	TGG	GCC	GAT	1080
Ala	Phe	Val	Gly	Phe	Val	Leu	Ser	Arg	Lys	Glu	Pro	Met	Trp	Ala	Asp	
305					310					315					320	
CTT	CTG	GCC	CTG	GCC	GCC	GCC	AGG	GGG	GGC	CGG	GTC	CAC	CGG	GCC	CCC	1128
Leu	Leu	Ala	Leu	Ala	Ala	Ala	Arg	Gly	Gly	Arg	Val	His	Arg	Ala	Pro	
				325					330					335		
GAG	CCT	TAT	AAA	GCC	CTC	AGG	GAC	CTG	AAG	GAG	GCG	CGG	GGG	CTT	CTC	1176
Glu	Pro	Tyr	Lys	Ala	Leu	Arg	Asp	Leu	Lys	Glu	Ala	Arg	Gly	Leu	Leu	
			340					345					350			
GCC	AAA	GAC	CTG	AGC	GTT	CTG	GCC	CTG	AGG	GAA	GGC	CTT	GGC	CTC	CCG	1224
Ala	Lys	Asp	Leu	Ser	Val	Leu	Ala	Leu	Arg	Glu	Gly	Leu	Gly	Leu	Pro	
		355					360					365				
CCC	GGC	GAC	GAC	CCC	ATG	CTC	CTC	GCC	TAC	CTC	CTG	GAC	CCT	TCC	AAC	1272
Pro	Gly	Asp	Asp	Pro	Met	Leu	Leu	Ala	Tyr	Leu	Leu	Asp	Pro	Ser	Asn	
		370				375					380					
ACC	ACC	CCC	GAG	GGG	GTG	GCC	CGG	CGC	TAC	GGC	GGG	GAG	TGG	ACG	GAG	1320
Thr	Thr	Pro	Glu	Gly	Val	Ala	Arg	Arg	Tyr	Gly	Gly	Glu	Trp	Thr	Glu	
385					390					395					400	
GAG	GCG	GGG	GAG	CGG	GCC	GCC	CTT	TCC	GAG	AGG	CTC	TTC	GCC	AAC	CTG	1368
Glu	Ala	Gly	Glu	Arg	Ala	Ala	Leu	Ser	Glu	Arg	Leu	Phe	Ala	Asn	Leu	
				405					410					415		
TGG	GGG	AGG	CTT	GAG	GGG	GAG	GAG	AGG	CTC	CTT	TGG	CTT	TAC	CGG	GAG	1416
Trp	Gly	Arg	Leu	Glu	Gly	Glu	Glu	Arg	Leu	Leu	Trp	Leu	Tyr	Arg	Glu	
			420					425					430			
GTG	GAG	AGG	CCC	CTT	TCC	GCT	GTC	CTG	GCC	CAC	ATG	GAG	GCC	ACG	GGG	1464
Val	Glu	Arg	Pro	Leu	Ser	Ala	Val	Leu	Ala	His	Met	Glu	Ala	Thr	Gly	
		435					440					445				
GTG	CGC	CTG	GAC	GTG	GCC	TAT	CTC	AGG	GCC	TTG	TCC	CTG	GAG	GTG	GCC	1512
Val	Arg	Leu	Asp	Val	Ala	Tyr	Leu	Arg	Ala	Leu	Ser	Leu	Glu	Val	Ala	
		450				455					460					
GAG	GAG	ATC	GCC	CGC	CTC	GAG	GCC	GAG	GTC	TTC	CGC	CTG	GCC	GGC	CAC	1560
Glu	Glu	Ile	Ala	Arg	Leu	Glu	Ala	Glu	Val	Phe	Arg	Leu	Ala	Gly	His	
465					470					475					480	
CCC	TTC	AAC	CTC	AAC	TCC	CGG	GAC	CAG	CTG	GAA	AGG	GTC	CTC	TTT	GAC	1608
Pro	Phe	Asn	Leu	Asn	Ser	Arg	Asp	Gln	Leu	Glu	Arg	Val	Leu	Phe	Asp	
				485				490						495		
GAG	CTA	GGG	CTT	CCC	GCC	ATC	GGC	AAG	ACG	GAG	AAG	ACC	GGC	AAG	CGC	1656
Glu	Leu	Gly	Leu	Pro	Ala	Ile	Gly	Lys	Thr	Glu	Lys	Thr	Gly	Lys	Arg	
			500					505					510			
TCC	ACC	AGC	GCC	GCC	GTC	CTG	GAG	GCC	CTC	CGC	GAG	GCC	CAC	CCC	ATC	1704
Ser	Thr	Ser	Ala	Ala	Val	Leu	Glu	Ala	Leu	Arg	Glu	Ala	His	Pro	Ile	
		515					520					525				
GTG	GAG	AAG	ATC	CTG	CAG	TAC	CGG	GAG	CTC	ACC	AAG	CTG	AAG	AGC	ACC	1752
Val	Glu	Lys	Ile	Leu	Gln	Tyr	Arg	Glu	Leu	Thr	Lys	Leu	Lys	Ser	Thr	
		530				535					540					

TAC Tyr 545	ATT Ile	GAC Asp	CCC Pro	TTG Leu	CCG Pro 550	GAC Asp	CTC Leu	ATC Ile	CAC His	CCC Pro 555	AGG Arg	ACG Thr	GGC Gly	CGC Arg	CTC Leu 560	1800
CAC His	ACC Thr	CGC Arg	TTC Phe	AAC Asn 565	CAG Gln	ACG Thr	GCC Ala	ACG Thr	GCC Ala 570	ACG Thr	GGC Gly	AGG Arg	CTA Leu	AGT Ser 575	AGC Ser	1848
TCC Ser	GAT Asp	CCC Pro	AAC Asn 580	CTC Leu	CAG Gln	AAC Asn	ATC Ile	CCC Pro 585	GTC Val	CGC Arg	ACC Thr	CCG Pro	CTT Leu 590	GGG Gly	CAG Gln	1896
AGG Arg	ATC Ile	CGC Arg 595	CGG Arg	GCC Ala	TTC Phe	ATC Ile	GCC Ala 600	GAG Glu	GAG Glu	GGG Gly	TGG Trp	CTA Leu 605	TTG Leu	GTG Val	GCC Ala	1944
CTG Leu 610	GAC Asp	TAT Tyr	AGC Ser	CAG Gln	ATA Ile	GAG Glu 615	CTC Leu	AGG Arg	GTG Val	CTG Leu 620	GCC Ala	CAC His	CTC Leu	TCC Ser	GGC Gly	1992
GAC Asp 625	GAG Glu	AAC Asn	CTG Leu	ATC Ile	CGG Arg 630	GTC Val	TTC Phe	CAG Gln	GAG Glu	GGG Gly 635	CGG Arg	GAC Asp	ATC Ile	CAC His	ACG Thr 640	2040
GAG Glu	ACC Thr	GCC Ala	AGC Ser	TGG Trp 645	ATG Met	TTC Phe	GGC Gly	GTC Val	CCC Pro 650	CGG Arg	GAG Glu	GCC Ala	GTG Val	GAC Asp 655	CCC Pro	2088
CTG Leu	ATG Met	CGC Arg 660	CGG Arg	GCG Ala	GCC Ala	AAG Lys	ACC Thr	ATC Ile 665	AAC Asn	TTC Phe	GGG Gly	GTC Val	CTC Leu 670	TAC Tyr	GGC Gly	2136
ATG Met	TCG Ser	GCC Ala 675	CAC His	CGC Arg	CTC Leu	TCC Ser	CAG Gln 680	GAG Glu	CTA Leu	GCC Ala	ATC Ile	CCT Pro 685	TAC Tyr	GAG Glu	GAG Glu	2184
GCC Ala 690	CAG Gln	GCC Ala	TTC Phe	ATT Ile	GAG Glu	CGC Arg 695	TAC Tyr	TTT Phe	CAG Gln	AGC Ser	TTC Phe 700	CCC Pro	AAG Lys	GTG Val	CGG Arg	2232
GCC Ala 705	TGG Trp	ATT Ile	GAG Glu	AAG Lys	ACC Thr 710	CTG Leu	GAG Glu	GAG Glu	GGC Gly	AGG Arg 715	AGG Arg	CGG Arg	GGG Gly	TAC Tyr	GTG Val 720	2280
GAG Glu	ACC Thr	CTC Leu	TTC Phe 725	GGC Arg	CGC Arg	CGC Arg	TAC Tyr 730	GTG Val	CCA Pro	GAC Asp	CTA Leu	GAG Glu	GCC Ala 735	CGG Arg		2328
GTG Val	AAG Lys	AGC Ser	GTG Val 740	CGG Arg	GAG Glu	GCG Ala	GCC Ala 745	GAG Glu	CGC Arg	ATG Met	GCC Ala	TTC Phe 750	AAC Asn	ATG Met	CCC Pro	2376
GTC Val	CAG Gln	GGC Gly 755	ACC Thr	GCC Ala	GCC Ala	GAC Asp 760	CTC Leu	ATG Met	AAG Lys	CTG Leu	GCT Ala	ATG Met 765	GTG Val	AAG Lys	CTC Leu	2424
TTC Phe 770	CCC Pro	AGG Arg	CTG Leu	GAG Glu	GAA Glu	ATG Met 775	GGG Gly	GCC Ala	AGG Arg	ATG Met 780	CTC Leu	CTT Leu	CAG Gln	GTC Val	CAC His	2472
GAC Asp 785	GAG Glu	CTG Leu	GTC Val	CTC Leu	GAG Glu	GCC Ala 790	CCA Pro	AAA Lys	GAG Glu	AGG Arg 795	GCG Ala	GAG Glu	GCC Ala	GTG Val	GCC Ala 800	2520
CGG Arg	CTG Leu	GCC Ala	AAG Lys	GAG Glu 805	GTC Val	ATG Met	GAG Glu	GGG Gly	GTG Val 810	TAT Tyr	CCC Pro	CTG Leu	GCC Ala	GTG Val	CCC Pro 815	2568

TGATACCACC 2626

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 832 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met 1	Arg	Gly	Met	Leu 5	Pro	Leu	Phe	Glu	Pro 10	Lys	Gly	Arg	Val	Leu 15	Leu
Val	Asp	Gly	His 20	His	Leu	Ala	Tyr	Arg 25	Thr	Phe	His	Ala	Leu 30	Lys	Gly
Leu	Thr	Thr 35	Ser	Arg	Gly	Glu	Pro 40	Val	Gln	Ala	Val	Tyr 45	Gly	Phe	Ala
Lys	Ser 50	Leu	Leu	Lys	Ala	Leu 55	Lys	Glu	Asp	Gly	Asp 60	Ala	Val	Ile	Val
Val 65	Phe	Asp	Ala	Lys	Ala 70	Pro	Ser	Phe	Arg	His 75	Glu	Ala	Tyr	Gly	Gly 80
Tyr	Lys	Ala	Gly	Arg 85	Ala	Pro	Thr	Pro	Glu 90	Asp	Phe	Pro	Arg	Gln 95	Leu
Ala	Leu	Ile	Lys 100	Glu	Leu	Val	Asp	Leu 105	Leu	Gly	Leu	Ala	Arg 110	Leu	Glu
Val	Pro	Gly 115	Tyr	Glu	Ala	Asp	Asp 120	Val	Leu	Ala	Ser	Leu 125	Ala	Lys	Lys
Ala	Glu 130	Lys	Glu	Gly	Tyr	Glu 135	Val	Arg	Ile	Leu	Thr 140	Ala	Asp	Lys	Asp
Leu 145	Tyr	Gln	Leu	Leu	Ser 150	Asp	Arg	Ile	His	Val 155	Leu	His	Pro	Glu	Gly 160
Tyr	Leu	Ile	Thr	Pro 165	Ala	Trp	Leu	Trp	Glu 170	Lys	Tyr	Gly	Leu	Arg 175	Pro
Asp	Gln	Trp	Ala 180	Asp	Tyr	Arg	Ala	Leu 185	Thr	Gly	Asp	Glu	Ser 190	Asp	Asn
Leu	Pro	Gly 195	Val	Lys	Gly	Ile	Gly 200	Glu	Lys	Thr	Ala	Arg 205	Lys	Leu	Leu
Glu	Glu 210	Trp	Gly	Ser	Leu	Glu 215	Ala	Leu	Leu	Lys	Asn 220	Leu	Asp	Arg	Leu
Lys 225	Pro	Ala	Ile	Arg	Glu 230	Lys	Ile	Leu	Ala	His 235	Met	Asp	Asp	Leu	Lys 240
Leu	Ser	Trp	Asp 245	Leu	Ala	Lys	Val	Arg	Thr 250	Asp	Leu	Pro	Leu	Glu 255	Val

Asp Phe Ala Lys Arg Arg Glu Pro Asp Arg Glu Arg Leu Arg Ala Phe
 260 265 270
 Leu Glu Arg Leu Glu Phe Gly Ser Leu Leu His Glu Phe Gly Leu Leu
 275 280 285
 Glu Ser Pro Lys Ala Leu Glu Glu Ala Pro Trp Pro Pro Pro Glu Gly
 290 295 300
 Ala Phe Val Gly Phe Val Leu Ser Arg Lys Glu Pro Met Trp Ala Asp
 305 310 315 320
 Leu Leu Ala Leu Ala Ala Ala Arg Gly Gly Arg Val His Arg Ala Pro
 325 330 335
 Glu Pro Tyr Lys Ala Leu Arg Asp Leu Lys Glu Ala Arg Gly Leu Leu
 340 345 350
 Ala Lys Asp Leu Ser Val Leu Ala Leu Arg Glu Gly Leu Gly Leu Pro
 355 360 365
 Pro Gly Asp Asp Pro Met Leu Leu Ala Tyr Leu Leu Asp Pro Ser Asn
 370 375 380
 Thr Thr Pro Glu Gly Val Ala Arg Arg Tyr Gly Gly Glu Trp Thr Glu
 385 390 395 400
 Glu Ala Gly Glu Arg Ala Ala Leu Ser Glu Arg Leu Phe Ala Asn Leu
 405 410 415
 Trp Gly Arg Leu Glu Gly Glu Glu Arg Leu Leu Trp Leu Tyr Arg Glu
 420 425 430
 Val Glu Arg Pro Leu Ser Ala Val Leu Ala His Met Glu Ala Thr Gly
 435 440 445
 Val Arg Leu Asp Val Ala Tyr Leu Arg Ala Leu Ser Leu Glu Val Ala
 450 455 460
 Glu Glu Ile Ala Arg Leu Glu Ala Glu Val Phe Arg Leu Ala Gly His
 465 470 475 480
 Pro Phe Asn Leu Asn Ser Arg Asp Gln Leu Glu Arg Val Leu Phe Asp
 485 490 495
 Glu Leu Gly Leu Pro Ala Ile Gly Lys Thr Glu Lys Thr Gly Lys Arg
 500 505 510
 Ser Thr Ser Ala Ala Val Leu Glu Ala Leu Arg Glu Ala His Pro Ile
 515 520 525
 Val Glu Lys Ile Leu Gln Tyr Arg Glu Leu Thr Lys Leu Lys Ser Thr
 530 535 540
 Tyr Ile Asp Pro Leu Pro Asp Leu Ile His Pro Arg Thr Gly Arg Leu
 545 550 555 560
 His Thr Arg Phe Asn Gln Thr Ala Thr Ala Thr Gly Arg Leu Ser Ser
 565 570 575
 Ser Asp Pro Asn Leu Gln Asn Ile Pro Val Arg Thr Pro Leu Gly Gln
 580 585 590
 Arg Ile Arg Arg Ala Phe Ile Ala Glu Glu Gly Trp Leu Leu Val Ala
 595 600 605

Leu Asp Tyr Ser Gln Ile Glu Leu Arg Val Leu Ala His Leu Ser Gly
 610 615 620
 Asp Glu Asn Leu Ile Arg Val Phe Gln Glu Gly Arg Asp Ile His Thr
 625 630 635 640
 Glu Thr Ala Ser Trp Met Phe Gly Val Pro Arg Glu Ala Val Asp Pro
 645 650 655
 Leu Met Arg Arg Ala Ala Lys Thr Ile Asn Phe Gly Val Leu Tyr Gly
 660 665 670
 Met Ser Ala His Arg Leu Ser Gln Glu Leu Ala Ile Pro Tyr Glu Glu
 675 680 685
 Ala Gln Ala Phe Ile Glu Arg Tyr Phe Gln Ser Phe Pro Lys Val Arg
 690 695 700
 Ala Trp Ile Glu Lys Thr Leu Glu Glu Gly Arg Arg Arg Gly Tyr Val
 705 710 715 720
 Glu Thr Leu Phe Gly Arg Arg Arg Tyr Val Pro Asp Leu Glu Ala Arg
 725 730 735
 Val Lys Ser Val Arg Glu Ala Ala Glu Arg Met Ala Phe Asn Met Pro
 740 745 750
 Val Gln Gly Thr Ala Ala Asp Leu Met Lys Leu Ala Met Val Lys Leu
 755 760 765
 Phe Pro Arg Leu Glu Glu Met Gly Ala Arg Met Leu Leu Gln Val His
 770 775 780
 Asp Glu Leu Val Leu Glu Ala Pro Lys Glu Arg Ala Glu Ala Val Ala
 785 790 795 800
 Arg Leu Ala Lys Glu Val Met Glu Gly Val Tyr Pro Leu Ala Val Pro
 805 810 815
 Leu Glu Val Glu Val Gly Ile Gly Glu Asp Trp Leu Ser Ala Lys Glu
 820 825 830

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 39 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGGTCCACGG CCTCCCGCGG GACGCCGAAC ATCCAGCTG

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 16 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

16

(2) INFORMATION FOR SEO ID NO:5:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

22

(2) INFORMATION FOR SEO ID NO:6:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

60

80

(2) INFORMATION FOR SEQ ID NO:7:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

37

(2) INFORMATION FOR SEQ ID NO:8:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

32

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTAAGGGATG GCTAGCTCCT GGGA

24

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CGCGCCGAAT TCCC

14

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 46 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCGCGGAAGC TTGGCTGCAG AATATTGCTA GCGGGAATTC GGCGCG

46